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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/508,997	06/27/2000	TOSHIO MIYATA	SHIM-004	5507

7590 09/25/2002  
KARL BOZICEVIC  
BOZICEVIC FIELD & FRANCIS  
200 MIDDLEFIELD ROAD  
SUITE 200  
MENLO PARK, CA 94025

EXAMINER

TURNER, SHARON L

ART UNIT PAPER NUMBER

1647

DATE MAILED: 09/25/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

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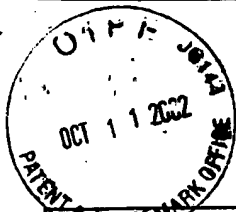
OCT 16 2002

TECH CENTER 1600/2900

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SEQUENT 10/25/02

LD 03/25/03



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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

Please find below a communication from the EXAMINER in charge of this application

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Turner whose telephone number is (703) 308-0056. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Gary Kunz whose telephone number is (703) 308-4623. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

*Sharon Turner*  
9-23-02



**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached, to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

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**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

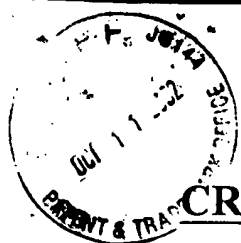
For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

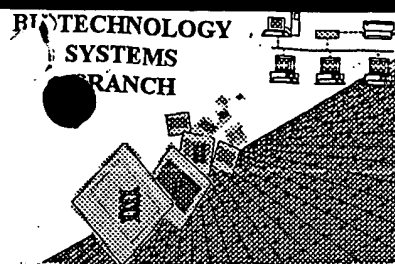
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

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165



#8  
D3  
2/7/02

647

## CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/508,997  
Filing Date: 6/27/2001  
Date Processed by STIC: 1/26/2002

STIC Contact: Mark Spencer, 703-308-4212

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OCT 16 2002

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FEB 05 2002  
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### Nature of Problem:

The CRF (was):

- ☒ (circle one) Damaged or Unreadable (for Unreadable, see attached)  
☐ Blank (no files on CRF) (see attached)  
☐ Empty file (filename present, but no bytes in file) (see attached)  
☐ Virus-infected. Virus name: \_\_\_\_\_ The STIC will not process the CRF.  
☐ Not saved in ASCII text  
☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.  
☐ Did not contain a Sequence Listing. (see attached sample)  
☐ Other: \_\_\_\_\_

**PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS.  
SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker>

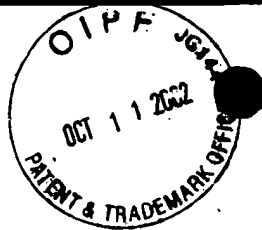
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel-Service , or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



## SEQUENCE LISTING

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&lt;110&gt; MIYATA, Toshio

&lt;120&gt; Megsin Protein

&lt;130&gt; SHIM-004

&lt;140&gt; 09/508,997

&lt;141&gt; 2000-06-27

&lt;150&gt; JP 09-275302

&lt;151&gt; 1997-09-22

&lt;160&gt; 44

&lt;170&gt; PatentIn Ver. 2.0

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 <213> Rattus rattus  
  
 <220>  
 <221> UNSURE  
 <222> 51, 94  
 <223> Xaa is unknown.

<400> 4  
 Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Gly Phe Asp Leu Phe  
 1 5 10 15

Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe Ser Ser  
 20 25 30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly  
 35 40 45

Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser  
 50 55 60

Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu  
 65 70 75 80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu  
 85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys  
 100 105 110  
 Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg  
 115 120 125  
 Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys  
 130 135 140  
 Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp  
 145 150 155 160  
 Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr  
 165 170 175  
 Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser  
 180 185 190  
 Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met  
 195 200 205  
 His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met  
 210 215 220  
 Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr Ile Met  
 225 230 235 240  
 Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln  
 245 250 255  
 Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val  
 260 265 270  
 Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg  
 275 280 285  
 Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg  
 290 295 300  
 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys  
 305 310 315 320  
 Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala  
 325 330 335  
 Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser  
 340 345 350  
 Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn  
 355 360 365  
 Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro  
 370 375 380

<210> 5  
 <211> 1147  
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1104)

<400> 5

ttc gac tta ttc aga gag atg gat agt agc caa gga aat gga aat gta	48
Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val	
1 5 10 15	
ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg	96
Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu	
20 25 30	
ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt	144
Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe	
35 40 45	
aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt	192
Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu	
50 55 60	
cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag	240
Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys	
65 70 75 80	
gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat	288
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr	
85 90 95	
gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct	336
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala	
100 105 110	
aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt	384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe	
115 120 125	
aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag	432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys	
130 135 140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg	480
Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val	
145 150 155 160	
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act	528
Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr	
165 170 175	
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta	576
Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val	
180 185 190	
gtt aat atg atg cat caa gaa cgg cgg ttc aat ttg tct acc att cag	624
Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln	
195 200 205	

cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc	672
Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser	
210 215 220	
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag	720
Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys	
225 230 235 240	
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa	768
Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys	
245 250 255	
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat	816
Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn	
260 265 270	
tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt	864
Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe	
275 280 285	
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc	912
Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu	
290 295 300	
tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag	960
Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu	
305 310 315 320	
ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag	1008
Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln	
325 330 335	
ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc	1056
Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val	
340 345 350	
atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct	1104
Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro	
355 360 365	
tgaaattcga tttggtttcc tatacagtaa caggcatcaa gaa	1147

<210> 6

<211> 368

<212> PRT

<213> Mus musculus

<400> 6

Phe Asp Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val
1 5 10 15

Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
20 25 30

Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu  
 50 55 60  
 Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys  
 65 70 75 80  
 Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr  
 85 90 95  
 Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala  
 100 105 110  
 Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe  
 115 120 125  
 Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys  
 130 135 140  
 Val Leu Gly Asp Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val  
 145 150 155 160  
 Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr  
 165 170 175  
 Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val  
 180 185 190  
 Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln  
 195 200 205  
 Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser  
 210 215 220  
 Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys  
 225 230 235 240  
 Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys  
 245 250 255  
 Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn  
 260 265 270  
 Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe  
 275 280 285  
 Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu  
 290 295 300  
 Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu  
 305 310 315 320  
 Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln  
 325 330 335  
 Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val  
 340 345 350  
 Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro

355

360

365

<210> 7  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 7  
tgtaaaacga cggccagt 18

<210> 8  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 8  
accatgatta cgccaagctt g 21

<210> 9  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 9  
tcagagaggt cattc 15

<210> 10  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 10  
tcattgatgg gtcctcaa 18

<210> 11  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 11  
agattcttga gctcagat 18

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 12  
aatggtggca taaacatg 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 13  
acagacaaat tgaacttc 18

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 14  
gaattcatgg cctcccttgc tgcagcaaa 29

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 15  
gtcgacttat caagggcaag aaactttgcc 30

<210> 16  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence:synthesis

<400> 16  
atgatctcag cattgtgaat g 21

<210> 17  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 17  
actgagggag ttgcttttct ac 22

<210> 18  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 18  
Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg  
1 5 10 15

<210> 19  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 19  
Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe  
1 5 10 15

<210> 20  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 20  
Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp  
1 5 10 15

<210> 21

<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 21  
Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu  
1 5 10 15

<210> 22  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 22  
atcggatcca tggcctccct tgctgcagca aatgcaga 38

<210> 23  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 23  
ataagctttc atcaagggca agaaactttg ccactgaata ag 42

<210> 24  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<221> misc feature  
<222> 26, 29  
<223> n is a or t or c or g.

<400> 24  
gtgaatgctg tgtacttaaa ggcaantgn 29

<210> 25  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<221> misc\_feature

<222> 3, 9, 15

<223> n is a or t or c or g.

<400> 25

aanagraang grtcngc

17

<210> 26

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<221> misc\_feature

<222> 6, 9, 12, 15, 18, 21

<223> n is a or t or c or g.

<400> 26

atggcntcng cngcngcngc naaygc

26

<210> 27

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 27

cgacctccag aggcaattcc agagagatca gccctgg

37

<210> 28

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 28

gtcttccaag cctacagatt tcaagtggt cctc

34

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 29  
 gctcagggca gtgaagatgc tcaggggaaga 30

<210> 30  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthesis

<400> 30  
 ctgacgtgca cagtcacctc gagcacc 27

<210> 31  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthesis

<400> 31  
 gaggtctcag aagaaggcac tgaggcaact gctgcc 36

<210> 32  
 <211> 19  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence:synthesis

<400> 32  
 ctctatagga gacacttgg 19

<210> 33  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:synthesis

<400> 33  
 gaaacaaatc aaagcaaac 19

<210> 34  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 34  
gaaattgaaa rcaarctgas yttycagaat

30

<210> 35  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 35  
ctgasyttyc agaatactaat ggamtgac

29

<210> 36  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 36  
ggaytsaggr agtwgctttt cwacratrtt

30

<210> 37  
<211> 36  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:synthesis

<400> 37  
gaggtctcag aggagggcac tgaagccact gctgcc

36

<210> 38  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthesis

<400> 38  
ccagtgcaga tctctctgga attgcctctg gaggtcgtc

39

<210> 39  
<211> 28  
<212> DNA  
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<220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 39  
 gcctgttact gtataggaaa ccaaaccg 28  
  
 <210> 40  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 40  
 atggcytccc tygctgcwgc raatgcagar tttkgc 36  
  
 <210> 41  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 41  
 atcggatcca tggcctccct tgct 24  
  
 <210> 42  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 42  
 ataagctttc atcatcaagg gcaag 25  
  
 <210> 43  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:synthesis  
  
 <400> 43  
 atggatccgc cgccatggcc tcccttgctg cagcaaatgc agag 44  
  
 <210> 44  
 <211> 27  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthesis

<400> 44

tatcctgagg cagtgttaac aagcaac

27